

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

<120> Therapeutic agent for chondroma and/or chondrosarcoma

<130> PH-1865-PCT

<150> JP 2002-334081

<151> 2002-11-18

<160> 85

<170> PatentIn Ver. 2.1

<210> 1

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Inventor; Yoshikawa, Hideki; Miyaji, Takahiro

<220>

<223> Description of Artificial Sequence: Synthetic DNA

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aaatagccct tgaccaggca

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<210> 2
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<223> Description of Artificial Sequence:Synthetic DNA

<400> 2
ctggttcggc ccacctctga aggttccaga atcgatag 38

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<400> 3
ggatcccggg ccagtgata gacagatg 28

<210> 4
<211> 29
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<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 4
ggatccggg tcagrggaag gtggrraaca 29

<210> 5
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<220>
<223> Description of Artificial Sequence: Synthetic DNA

<400> 5
gttttcccag tcacgac 17

<210> 6
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<400> 6
caggaaacag ctatgac 17

<210> 7
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<223> Description of Artificial Sequence:Synthetic DNA

<400> 7

gtcttaagctt ccaccatgaa acttcgggct c

31

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 8

tgttggatcc ctgcagagac agtgaccaga

30

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 9

gtctgaattc aagcttccac catggggttt gggctg

36

<210> 10
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<212> DNA
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<400> 10
tttcccgggc ccttggtgga ggctgaggag acggtgacca g 41

<210> 11
<211> 109
<212> DNA
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<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 11
gtctgaattc aagcttagta ctggccagc ccaaggccaa ccccacggtc accctgttcc 60
cgccctcctc tgaggagctc caagccaaca aggccacact agtgtgtct 109

<210> 12
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<223> Description of Artificial Sequence:Synthetic DNA

<400> 12

ggtttgggtgg tctccactcc cgccttgacg gggctgccat ctgccttcca ggccactgtc 60
acagctcccg ggttagaagtc actgatcaga cacactagtg tggccttgtt 110

<210> 13

<211> 98

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 13

ggagtggaga ccaccaaacc ctccaaacag agcaacaaca agtacgcggc cagcagctac 60
ctgagcctga cgcccgagca gtggaagtcc cacagaag 98

<210> 14

<211> 106

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

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catgcgtgac ctggcagctg tagttctgt gggacttcca ctgctc

106

<210> 15

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 15

gtctgaattc aagcttagta cttggccagc ccaaggccaa ccc

43

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 16

tgttgaattc ttactatgaa

20

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 17

caacaagtac gcggccagca gctacacctgag cctgacgc

39

<210> 18

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 18

gtagctgctg gccgcgtact ttttgttgc ctgtttgga

39

<210> 19

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 19

gtctgaattc aagcttagtc ctaggtcgaa ctgtggctgc accatc

46

<210> 20

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 20

tgttgaattc ttactaacac tctccctgt tgaa

34

<210> 21

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 21

gtctaagctt ccaccatggc ctggactcct ctctt

35

<210> 22

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 22

tgttgaattc agatctaact acttacctag gacagtgacc ttggtccc 48

<210> 23

<211> 128

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 23

gtctaagctt ccaccatggg gtttgggctg agctgggttt tcctcggtgc tcttttaaga 60
ggtgtccagt gtcaggtgca gctgggtggag tctgggggag gcgtggtcca gcctgggagg 120
tccctgag 128

<210> 24

<211> 125

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Synthetic DNA

<400> 24

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atctccagag acaattccaa gaacacgctg tatctgcaaa tgaacagcct gagagctgag 120
gacac 125

<210> 25
<211> 132
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 25
ctaccaccac tactaatggc tgccacccac tccagcccct gcctggagc ctggcgacc 60
caagacatgc catagctact gaaggtaat ccagaggctg cacaggagag tctcagggac 120
ctcccaggct gg 132

<210> 26
<211> 110
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 26
tggatcc ctgaggagac ggtgaccagg gttccctggc cccagtaagc aaagtaagtc 60
atagtagtct gtctcgaca gtaatacaca gccgtgtcct cagctctcag 110

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 27

gtctaagctt ccaccatggg gtttgggctg 30

<210> 28

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 28

tgttggatcc ctgaggagac ggtgaccagg 30

<210> 29

<211> 133

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 29

acaaagcttc caccatggcc tggactcctc tcttcttctt ctttgttctt cattgctcag 60
gttctttctc ccagcttgc ctgactcaat cgccctctgc ctctgcctcc ctgggagcct 120

cggtaagct cac

133

<210> 30

<211> 118

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 30

agcaagatgg aagccacagc acaggtgatg ggattcctga tcgcttctca ggctccagct 60
ctggggctga gcgcgtacctc accatctcca gcctccagtc tgaggatgag gctgacta 118

<210> 31

<211> 128

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 31

ctgtggcttc catcttgctt aagtttcatc aagtaccgag ggcccttctc tggctgctgc 60
tgatgccatt caatggtgta cgtactgtgc tgactactca aggtgcaggt gagcttgacc 120
gaggctcc 128

<210> 32

<211> 114

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 32

cttggatccg ggctgaccta ggacggtcag tttggtcctt ccggcgaaca ccctcacaaa 60
ttgttcctta attgtatcac ccacaccaca gtaatagtca gcctcatcct caga 114

<210> 33

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 33

acaaagcttc caccatg 17

<210> 34

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 34

cttggatccg ggctgacct

19

<210> 35

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 35

cttggatccg ggctgaccta ggacggtcag tttggtcctt ccggcgaaca cgtacacaaa 60
ttgttcctta attgt 75

<210> 36

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 36

aaaggatcct taagatccat caagtaccga gggggcttct ctg

43

<210> 37

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 37

acaaagctta gcgctacctc accatctcca gcctccagcc tgagga 46

<210> 38

<211> 111

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 38

cttggatccg ggctgaccta ggacggtcag tttggtcctt ccggcgaaca cgtacacaaa 60
ttgttcctta attgtatcac ccacaccaca gatatagtca gcctcatcct c 111

<210> 39

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 39

cttctctggc tgctgctgat accattcaat ggtgtacgta ct 42

<210> 40

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 40

cgagggccct tctctggctg ctgctg 26

<210> 41

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 41

gagaagggcc ctargtacst gatgrawctt aagca 35

<210> 42

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 42

cacgaattca ctatcgattc tggaaccttc agagg

35

<210> 43

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 43

ggcttggagc tcctcaga

18

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 44

gacagtggtt caaagtttt

20

<210> 45

<211> 118

<212> PRT

<213> Mus musculus

<400> 45

Gln Leu Val Leu Thr Gln Ser Ser Ser Ala Ser Phe Ser Leu Gly Ala

1 5 10 15

Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr

20 25 30

Ile Glu Trp Tyr Gln Gln Pro Leu Lys Pro Pro Lys Tyr Val Met

35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp

50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Asp Arg Tyr Leu Ser Ile Ser

65 70 75 80

Asn Ile Gln Pro Glu Asp Glu Ala Met Tyr Ile Cys Gly Val Gly Asp

85 90 95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Val

100 105 110

Thr Val Leu Gly Gln Pro

115

<210> 46

<211> 118

<212> PRT

<213> Mus musculus

<400> 46

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly

1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met Ser Trp Ile Arg Gln Thr Pro Asp Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys
85 90 95
Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ala
115

<210> 47
<211> 116
<212> PRT
<213> Homo sapiens

<400> 47
Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30
Ile Glu Trp His Gln Gln Gln Pro Glu Lys Gly Pro Arg Tyr Leu Met
35 40 45
Lys Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp

50	55	60	
Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser			
65	70	75	80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp			
85	90	95	
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu			
100	105	110	
Thr Val Leu Gly			
115			

<210> 48

<211> 118

<212> PRT

<213> Homo sapiens

<400> 48

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala			
1	5	10	15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr			
20	25	30	

Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Leu Met			
35	40	45	

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp			
50	55	60	

Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser			
65	70	75	80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp			
85	90	95	

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu Gly Gln Pro
115

<210> 49

<211> 118

<212> PRT

<213> Homo sapiens

<400> 49

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15

Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30

Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Val Met
35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp
85 90 95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu Gly Gln Pro
115

<210> 50

<211> 118

<212> PRT

<213> Homo sapiens

<400> 50

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala

1

5

10

15

Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr

20

25

30

Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg Tyr Leu Met

35

40

45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp

50

55

60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser

65

70

75

80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp

85

90

95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu

100

105

110

Thr Val Leu Gly Gln Pro

115

<210> 51

<211> 118

<212> PRT

<213> Homo sapiens

<400> 51

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala

1 5 10 15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30
Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg Tyr Val Met
35 40 45
Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60
Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Val Gly Asp
85 90 95
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Thr Lys Leu
100 105 110
Thr Val Leu Gly Gln Pro
115

<210> 52
<211> 118
<212> PRT
<213> Homo sapiens

<400> 52
Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30
Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Leu Met
35 40 45
Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp

50 55 60
Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp
85 90 95
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu
100 105 110
Thr Val Leu Gly Gln Pro
115

<210> 53

<211> 118

<212> PRT

<213> Homo sapiens

<400> 53

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala
1 5 10 15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
20 25 30
Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg Tyr Leu Met
35 40 45
Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
50 55 60
Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser
65 70 75 80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp
85 90 95
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu

	100	105	110
Thr Val Leu Gly Gln Pro			
	115		
<210> 54			
<211> 118			
<212> PRT			
<213> Homo sapiens			
<400> 54			
Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala			
1	5	10	15
Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr			
20	25	30	
Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Lys Tyr Val Met			
35	40	45	
Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp			
50	55	60	
Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser			
65	70	75	80
Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp			
85	90	95	
Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly Thr Lys Leu			
100	105	110	
Thr Val Leu Gly Gln Pro			
	115		

<210> 55

<211> 118

<212> PRT

<213> Homo sapiens

<400> 55

Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala

1 5 10 15

Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr

20 25 30

Ile Glu Trp Tyr Gln Gln Pro Glu Lys Gly Pro Arg Tyr Val Met

35 40 45

Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp

50 55 60

Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu Thr Ile Ser

65 70 75 80

Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly Val Gly Asp

85 90 95

Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Thr Lys Leu

100 105 110

Thr Val Leu Gly Gln Pro

115

<210> 56

<211> 118

<212> PRT

<213> Homo sapiens

<400> 56

Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30
Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly Gln Gly Thr
100 105 110
Leu Val Thr Val Ser Ser
115

<210> 57

<211> 411

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 57

atg aac ttc ggg ctc agc ttg att ttc ctt gcc ctc att tta aaa ggt			48
Met Asn Phe Gly Leu Ser Leu Ile Phe Leu Ala Leu Ile Leu Lys Gly			
	-15	-10	-5
gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga gac tta gtg aag			96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys			
	-1	5	10
cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc			144
Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe			
	15	20	25
agt agc tat ggc atg tct tgg att cgc cag act cca gac aag agg ctg			192
Ser Ser Tyr Gly Met Ser Trp Ile Arg Gln Thr Pro Asp Lys Arg Leu			
	30	35	40
gag tgg gtc gca acc att agt agt ggt ggt agt tac acc tac tat cca			240
Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro			
	50	55	60
gac agt gtg aag ggg cga ttc acc atc tcc aga gac aat gcc aag aac			288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn			
	65	70	75
acc cta tac ctg caa atg agc agt ctg aag tct gag gac aca gcc atg			336
Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met			
	80	85	90
ttt tac tgt gca aga cag act act atg act tac ttt gct tac tgg ggc			384
Phe Tyr Cys Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly			
	95	100	105
caa ggg act ctg gtc act gtc tct gca			411
Gln Gly Thr Leu Val Thr Val Ser Ala			
	110	115	

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 58

atg	ggg	ttt	ggg	ctg	agc	tgg	gtt	ttc	ctc	gtt	gct	ctt	tta	aga	ggt	48
Met	Gly	Phe	Gly	Leu	Ser	Trp	Val	Phe	Leu	Val	Ala	Leu	Leu	Arg	Gly	
																-5
																-10
																-15
gtc	cag	tgt	cag	gtg	cag	ctg	gtg	gag	tct	ggg	gga	ggc	gtg	gtc	cag	96
Val	Gln	Cys	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	
																10
																-1
cct	ggg	agg	tcc	ctg	aga	ctc	tcc	tgt	gca	gcc	tct	gga	ttc	acc	ttc	144
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	
																20
																15
agt	agc	tat	ggc	atg	tct	tgg	gtc	cgc	cag	gct	cca	ggc	aag	ggg	ctg	192
Ser	Ser	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
																35
																40
gag	tgg	gtg	gca	acc	att	agt	agt	ggt	agt	tac	acc	tac	tat	cca		240
Glu	Trp	Val	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Tyr	Thr	Tyr	Tyr	Pro	
																50
																55
																60
gac	agt	gtg	aag	ggg	cga	ttc	acc	atc	tcc	aga	gac	aat	tcc	aag	aac	288

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75
acg ctg tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
80 85 90
tat tac tgt gcg aga cag act act atg act tac ttt gct tac tgg ggc 384
Tyr Tyr Cys Ala Arg Gln Thr Thr Met Thr Tyr Phe Ala Tyr Trp Gly
95 100 105
cag gga acc ctg gtc acc gtc tcc tca 411
Gln Gly Thr Leu Val Thr Val Ser Ser
110 115

<210> 59

<211> 11

<212> PRT

<213> Homo sapiens

<400> 59

Lys Ala Ser Gln Asp Val Asn Thr Ala Val Ala

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<213> Homo sapiens

<400> 60

Ser Ala Ser Asn Arg Tyr Thr

1 5

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<211> 9

<212> PRT

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Gln Gln His Tyr Ser Thr Pro Phe Thr

1 5

<210> 62

<211> 5

<212> PRT

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<400> 62

Pro Tyr Trp Met Gln

1 5

<210> 63

<211> 16

<212> PRT

<213> Homo sapiens

<400> 63

Ser Ile Phe Gly Asp Gly Asp Thr Arg Tyr Ser Gln Lys Phe Lys Gly

1 5 10 15

<210> 64

<211> 11

<212> PRT

<213> Homo sapiens

<400> 64

Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr

1 5 10

<210> 65

<211> 411

<212> DNA

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<220>

<221> CDS

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<220>

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<222> (58)..(411)

<400> 65

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-15 -10 -5

tct ttc tcc caa ctt gtg ctc act cag tca tct tca gcc tct ttc tcc 96

Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Ser Ser Ala Ser Phe Ser

-1 1 5 10

ctg gga gcc tca gca aaa ctc acg tgc acc ttg agt agt cag cac agt 144

Leu Gly Ala Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser
 15 20 25
 acg tac acc att gaa tgg tat cag caa cag cca ctc aag cct cct aag 192
 Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Leu Lys Pro Pro Lys
 30 35 40 45
 tat gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240
 Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
 50 55 60
 att cct gat cgc ttc tct gga tcc agc tct ggt gct gat cgc tac ctt 288
 Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Asp Arg Tyr Leu
 65 70 75
 agc att tcc aac atc cag cca gaa gat gaa gca atg tac atc tgt ggt 336
 Ser Ile Ser Asn Ile Gln Pro Glu Asp Glu Ala Met Tyr Ile Cys Gly
 80 85 90
 gtg ggt gat aca att aag gaa caa ttt gtg tat gtt ttc ggc ggt ggg 384
 Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly
 95 100 105
 acc aag gtc act gtc cta ggt cag ccc 411
 Thr Lys Val Thr Val Leu Gly Gln Pro
 110 115

<210> 66

<211> 411

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<220>

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<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 66

atg gcc tgg act cct ctc ttc ttc ttc ttt gtt ctt cat tgc tca ggt 48

Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly

-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96

Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144

Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15 20 25

acg tac acc att gaa tgg cat cag cag cca gag aag ggc cct cgg 192

Thr Tyr Thr Ile Glu Trp His Gln Gln Gln Pro Glu Lys Gly Pro Arg

30 35 40 45

tac ttg atg aaa ctt aag caa gat gga agc cac agc aca ggt gat ggg 240

Tyr Leu Met Lys Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly

50 55 60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288

Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu

65 70 75

acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt 336

Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly

80 85 90

gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384

Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly

95	100	105	
acc aaa ctg acc gtc cta ggt cag ccc			411
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110	115		
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tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc			96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser			
-1	1	5	10
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt			144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15	20	25	
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag			192

Thr	Tyr	Thr	Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	Lys	Gly	Pro	Lys	
30										40					45	
tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg															240	
Tyr	Leu	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
									55					60		
50																
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu	
65								70						75		
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	tac	tgt	ggt	336
Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	
80								85				90				
gtg	ggt	gat	aca	att	aag	gaa	caa	ttt	gtg	tac	gtg	ttc	ggc	gga	ggg	384
Val	Gly	Asp	Thr	Ile	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
95								100				105				
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ccc							411	
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro								
110								115								

<210> 68

<211> 411

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<213> Homo sapiens

<220>

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<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 68

atg gcc tgg act cct ctc ttc ttc ttc ttt gtt ctt cat tgc tca ggt 48
Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly
-15 -10 -5
tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser
-1 1 5 10
ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser
15 20 25
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys
30 35 40 45
tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
50 55 60
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu
65 70 75
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt 336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly
80 85 90
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
95 100 105
acc aaa ctg acc gtc cta ggc cag ccc 411
Thr Lys Leu Thr Val Leu Gly Gln Pro

110

115

<210> 69

<211> 411

<212> DNA

<213> Homo sapiens

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<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 69

atg gcc tgg act cct ctc ttc ttc ttc ttt gtt ctt cat tgc tca ggt 48

Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly

-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96

Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144

Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg 192

Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Arg

30 35 40 45

tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240

Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
50 55 60
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu
65 70 75
acc atc tcc agc ctc cag tct gag gat gag gct gac tat tac tgt ggt 336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly
80 85 90
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
95 100 105
acc aaa ctg acc gtc cta ggc cag ccc 411
Thr Lys Leu Thr Val Leu Gly Gln Pro
110 115

<210> 70

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 70

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			-15						-10					-5		
tct	ttc	tcc	cag	ctt	gtg	ctg	act	caa	tcg	ccc	tct	gcc	tct	gcc	96	
Ser	Phe	Ser	Gln	Leu	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ala	Ser	Ala	Ser	
			-1	1			5						10			
ctg	gga	gcc	tcg	gtc	aag	ctc	acc	tgc	acc	ttg	agt	agt	cag	cac	agt	144
Leu	Gly	Ala	Ser	Val	Lys	Leu	Thr	Cys	Thr	Leu	Ser	Ser	Gln	His	Ser	
			15				20						25			
acg	tac	acc	att	gaa	tgg	tat	cag	cag	cag	cca	gag	aag	ggc	cct	agg	192
Thr	Tyr	Thr	Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	Lys	Gly	Pro	Arg	
			30				35						40		45	
tac	gtg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
Tyr	Val	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
			50				55						60			
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu		
			65				70						75			
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	tac	tgt	ggt	336
Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gly	
			80				85						90			
gtg	ggt	gat	aca	att	aag	gaa	caa	ttt	gtg	tac	gtg	ttc	ggc	gga	ggg	384
Val	Gly	Asp	Thr	Ile	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
			95				100						105			
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ccc								411
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro								
			110				115									

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 71

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Met Ala Trp Thr Pro Leu Phe Phe Phe Val Leu His Cys Ser Gly

-15

-10

-5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96

Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1

5

10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144

Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser

15

20

25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192

Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys

30

35

40

45

tac ctg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240

Tyr Leu Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly

50

55

60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288

Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr Leu
65 70 75
acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt 336
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly
80 85 90
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
95 100 105
acc aaa ctg acc gtc cta ggc cag ccc 411
Thr Lys Leu Thr Val Leu Gly Gln Pro
110 115

<210> 72

<211> 411

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 72

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-15 -10 -5

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Ser	Phe	Ser	Gln	Leu	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ala	Ser	Ala	Ser	
-1	1					5						10				
ctg	gga	gcc	tcg	gtc	aag	ctc	acc	tgc	acc	ttg	agt	agt	cag	cac	agt	144
Leu	Gly	Ala	Ser	Val	Lys	Leu	Thr	Cys	Thr	Leu	Ser	Ser	Gln	His	Ser	
15						20						25				
acg	tac	acc	att	gaa	tgg	tat	cag	cag	cag	cca	gag	aag	ggc	cct	agg	192
Thr	Tyr	Thr	Ile	Glu	Trp	Tyr	Gln	Gln	Gln	Pro	Glu	Lys	Gly	Pro	Arg	
30						35				40				45		
tac	ctg	atg	gat	ctt	aag	caa	gat	gga	agc	cac	agc	aca	ggt	gat	ggg	240
Tyr	Leu	Met	Asp	Leu	Lys	Gln	Asp	Gly	Ser	His	Ser	Thr	Gly	Asp	Gly	
						50			55			60				
att	cct	gat	cgc	ttc	tca	ggc	tcc	agc	tct	ggg	gct	gag	cgc	tac	ctc	288
Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Gly	Ala	Glu	Arg	Tyr	Leu		
65						70						75				
acc	atc	tcc	agc	ctc	cag	tct	gag	gat	gag	gct	gac	tat	atc	tgt	ggt	336
Thr	Ile	Ser	Ser	Leu	Gln	Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Ile	Cys	Gly	
80						85						90				
gtg	ggt	gat	aca	att	aag	gaa	caa	ttt	gtg	tac	gtg	ttc	ggc	gga	ggg	384
Val	Gly	Asp	Thr	Ile	Lys	Glu	Gln	Phe	Val	Tyr	Val	Phe	Gly	Gly	Gly	
95						100						105				
acc	aaa	ctg	acc	gtc	cta	ggc	cag	ccc								411
Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro								
110						115										

<210> 73

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 73

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-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96
Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser
-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg agt agt cag cac agt 144
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser
15 20 25

acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct aag 192
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Lys
30 35 40 45

tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg 240
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly
50 55 60

att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc 288
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu
65 70 75

acc atc tcc agc ctc cag tct gag gat gag gag gct gac tat atc tgt ggt 336

Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly
80 85 90
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg 384
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly
95 100 105
acc aaa ctg acc gtc cta ggc cag ccc 411
Thr Lys Leu Thr Val Leu Gly Gln Pro
110 115

<210> 74

<211> 411

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(411)

<220>

<221> mat_peptide

<222> (58)..(411)

<400> 74

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-15 -10 -5

tct ttc tcc cag ctt gtg ctg act caa tcg ccc tct gcc tct gcc tcc 96

Ser Phe Ser Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala Ser

-1 1 5 10

ctg gga gcc tcg gtc aag ctc acc tgc acc ttg	agt agt cag cac agt	144	
Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser			
15	20	25	
acg tac acc att gaa tgg tat cag cag cag cca gag aag ggc cct agg		192	
Thr Tyr Thr Ile Glu Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro Arg			
30	35	40	45
tac gtg atg gat ctt aag caa gat gga agc cac agc aca ggt gat ggg		240	
Tyr Val Met Asp Leu Lys Gln Asp Gly Ser His Ser Thr Gly Asp Gly			
50	55	60	
att cct gat cgc ttc tca ggc tcc agc tct ggg gct gag cgc tac ctc		288	
Ile Pro Asp Arg Phe Ser Gly Ser Ser Gly Ala Glu Arg Tyr Leu			
65	70	75	
acc atc tcc agc ctc cag tct gag gat gag gct gac tat atc tgt ggt		336	
Thr Ile Ser Ser Leu Gln Ser Glu Asp Glu Ala Asp Tyr Ile Cys Gly			
80	85	90	
gtg ggt gat aca att aag gaa caa ttt gtg tac gtg ttc ggc gga ggg		384	
Val Gly Asp Thr Ile Lys Glu Gln Phe Val Tyr Val Phe Gly Gly Gly			
95	100	105	
acc aaa ctg acc gtc cta ggc cag ccc		411	
Thr Lys Leu Thr Val Leu Gly Gln Pro			
110	115		

<210> 75

<211> 34

<212> PRT

<213> Homo sapiens

<400> 75

Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly Lys Ser Ile Gln

1 5 10 15
Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile Ala Glu Ile His
20 25 30
Thr Ala

<210> 76
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 76
cagatgcacc tgacgccctt 20

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 77
cccagccgtg gttatcctgg a 21

<210> 78
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 78
gtccaccaag aagctgagcg 20

<210> 79
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 79
ttggtgacaca gggcctttag 20

<210> 80
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 80

cagggaaaacc aggtctcgat g

21

<210> 81

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 81

ttgaggccct tagttgctat g

21

<210> 82

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Synthetic DNA

<400> 82

agagtgcgtc cccatctgcc caactgacct

30

<210> 83
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

<400> 83
cattactccc aactgggcgc caccaggcctt 30

<210> 84
<211> 22
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic DNA

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<210> 85
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 85

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21